Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims

1. (Currently pending) A method for analysing a heterogeneous sample of peptides, or protein or peptide fragments, the method comprising:

   (a) separating the heterogeneous sample of peptides, or protein or peptide fragments, into heterogeneous classes by binding members of each class to a spaced apart defined location on an array, wherein members of each class have a motif common to that class; and

   (b) characterising the peptides, or protein or peptide fragments, in each class by determining the mass of the peptides, or protein or peptide fragments in the heterogenous classes, and determining the abundance of peptides, or protein or peptide fragments, of different mass in the heterogeneous classes.

2. (Currently pending) A method according to Claim 1 wherein the heterogeneous sample of peptides, or protein or peptide fragments, is an extract of the total protein content of a cell or tissue type.

3. (Currently pending) A method according to Claim 1 wherein, prior to performing step (a), the heterogeneous sample of fragments is formed by fragmenting a heterogeneous sample of proteins or peptides.

4. (Currently pending) A method according to Claim 3 wherein the fragmenting is performed by chemical or enzymatic cleavage.

5. (Currently pending) A method according to Claim 3 wherein the fragmenting is performed using a sequence-directed cleavage mechanism.

6. (Currently pending) A method according to Claim 3 wherein the fragmenting is performed by digestion of the heterogeneous sample of proteins or peptides with trypsin.

7. (Currently pending) A method according to claim 1 wherein the motif in each peptide, or protein or peptide fragment, is at the same location in each peptide, or